



DR N-PSDB; AAQ96297.

XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
PT for identifying antagonists and for treating diseases characterised by  
PT monocyte infiltrates.

XX Claim 2; Fig 1; 84pp; English.

CC To identify and clone new members of the chemokine receptor gene family,  
CC degenerate oligo primers were designed corresp. to the conserved  
CC sequences R79167 in the second and R79168 in the third transmembrane  
CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the  
CC HUMSRS orphan receptor (Genbank Accession #U92933. The degenerate oligo  
CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
CC yielded a number of PCR products. One cDNA appeared to encode a novel  
CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
CC library was constructed in pPROG and probed with the PCR product. A 2.1  
CC kb cDNA clone was obtcd. Analysis of additional clones in the MM6 cDNA  
CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
CC transmembrane domain but contained a different cytoplasmic tail. The  
CC second sequence appears to represent alternative splicing of the carboxyl  
CC-terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
CC-1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-  
CC-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX Sequence 374 AA;

XX Query Match 100.0%; Score 1970; DB 2; Length 374;

XX Best Local Similarity 100.0%; Pred. No. 5.1e-215; Mismatches 0; Indels 0; Gaps 0;

XX Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISTSRSRIRNTNNGSEVYTFEDYDGAPECHKEDVKGQGLPPLYSLVIFGFVGN 60

DB 1 MISTSRSRIRNTNNGSEVYTFEDYDGAPECHKEDVKGQGLPPLYSLVIFGFVGN 60

QY 61 MIVVILINCKKLCCTDIYLLNLAIISDLFLITPLMHSANENWVFNACCKLFTGLY 120

DB 61 MIVVILINCKKLCCTDIYLLNLAIISDLFLITPLMHSANENWVFNACCKLFTGLY 120

QY 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

DB 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

QY 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

DB 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

QY 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWICVSGILKTLRCRNEKKRR 240

DB 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWICVSGILKTLRCRNEKKRR 240

QY 241 AVRVIPTIMIVYFLFMTPNIVILNTFOEFGLSNCESTSDQDQATQVTEILGMHCCI 300

DB 241 AVRVIPTIMIVYFLFMTPNIVILNTFOEFGLSNCESTSDQDQATQVTEILGMHCCI 300

QY 301 NPIIYAVGEKRSLEPHIALGCRAPLQKPVCGPGVPRGKNVKTTOGLDGRGKSKI 360

DB 301 NPIIYAVGEKRSLEPHIALGCRAPLQKPVCGPGVPRGKNVKTTOGLDGRGKSKI 360

QY 361 GRAPEASLQDKGA 374

DB 361 GRAPEASLQDKGA 374

QY 361 GRAPEASLQDKGA 374

DB 361 GRAPEASLQDKGA 374

QY 361 GRAPEASLQDKGA 374

DB 361 GRAPEASLQDKGA 374

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
XX chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
XX antineoplastic; antineoplastic; immunosuppressive; dermatological;  
XX antineoplastic; antineoplastic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IIPP-) IFF PHARM GMBH.

XX (FORS/) FORSMANN U.

XX Forsmann W, Adermann K, Helldorf A, Spodberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful  
XX for detecting tumors, inflammation etc., also therapeutic use of ligand  
XX inhibitors.

XX Disclosure; Page 9; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least  
XX two different ligands (I) for receptors (II) that are implicated in  
XX disease. (A) are used for the diagnosis of tumors (especially colorectal  
XX or prostatic), organ rejection, inflammation and autoimmune diseases.  
XX Also inhibitors of (I) are used therapeutically against tumors (and their  
XX metastases), inflammation (particularly bronchial asthma or chronic bowel  
XX inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
XX where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
XX endocrine, motor or urogenital systems or skin are affected, and bone  
XX marrow diseases. The products of the invention are chemokine derivatives  
XX which have cytostatic, antiinflammatory, antineoplastic, antineoplastic,  
XX immunosuppressive, dermatological, antineoplastic, antineoplastic.  
XX Chemokines act on specific tumor and inflammatory cells through a  
XX constellation of chemokine receptors (CR), which control migration and  
XX proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
XX fragments used to illustrate the method of the invention

XX Sequence 374 AA;

XX Query Match 100.0%; Score 1970; DB 4; Length 374;

XX Best Local Similarity 100.0%; Pred. No. 5.1e-215; Mismatches 0; Indels 0; Gaps 0;

XX Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISTSRSRIRNTNNGSEVYTFEDYDGAPECHKEDVKGQGLPPLYSLVIFGFVGN 60

DB 1 MISTSRSRIRNTNNGSEVYTFEDYDGAPECHKEDVKGQGLPPLYSLVIFGFVGN 60

QY 61 MIVVILINCKKLCCTDIYLLNLAIISDLFLITPLMHSANENWVFNACCKLFTGLY 120

DB 61 MIVVILINCKKLCCTDIYLLNLAIISDLFLITPLMHSANENWVFNACCKLFTGLY 120

QY 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

DB 121 HIGYFGIIFILLITDRYLAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

QY 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWICVSGILKTLRCRNEKKRR 240

DB 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWICVSGILKTLRCRNEKKRR 240

QY 241 AVRVIPTIMIVYFLFMTPNIVILNTFOEFGLSNCESTSDQDQATQVTEILGMHCCI 300

DB 241 AVRVIPTIMIVYFLFMTPNIVILNTFOEFGLSNCESTSDQDQATQVTEILGMHCCI 300

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 21:10:05 ; Search time 43 Seconds

(without alignments)  
649,273 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970  
Sequence: 1 M1STSRSRIRNTNNGEEVY.....GKGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/1/aa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/aa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/aa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	374	1 US-08-450-393A-2	Sequence 2, Appl1
2	1970	100.0	374	3 US-08-446-669-2	Sequence 2, Appl1
3	1970	100.0	374	4 US-10-039-659A-14	Sequence 14, Appl1
4	1970	100.0	374	4 US-09-625-573-2	Sequence 2, Appl1
5	1970	100.0	374	5 PCT-US95-00476-2	Sequence 2, Appl1
6	1970	100.0	374	4 US-09-949-016-11222	Sequence 1122, A
7	1823	92.5	344	3 US-08-466-943D-9	Sequence 9, Appl1
8	1823	92.5	344	4 US-09-502-784A-9	Sequence 9, Appl1
9	1727.5	87.7	329	4 US-09-502-783A-9	Sequence 9, Appl1
10	1727.5	87.7	329	4 US-09-339-812A-9	Sequence 9, Appl1
11	1727.5	87.7	329	4 US-09-195-662A-9	Sequence 9, Appl1
12	1651.5	83.8	360	1 US-08-450-393A-4	Sequence 4, Appl1
13	1651.5	83.8	360	1 US-08-446-669-4	Sequence 4, Appl1
14	1651.5	83.8	360	3 US-09-045-583-50	Sequence 50, Appl1
15	1651.5	83.8	360	3 US-09-534-185-50	Sequence 50, Appl1
16	1651.5	83.8	360	4 US-09-131-827A-2	Sequence 2, Appl1
17	1651.5	83.8	360	4 US-09-625-573-4	Sequence 4, Appl1
18	1651.5	83.8	360	5 PCT-US95-00476-4	Sequence 4, Appl1
19	1651.5	83.8	377	4 US-09-949-016-11221	Sequence 1121, A
20	1650.5	83.8	360	4 US-09-131-827A-20	Sequence 20, Appl1
21	1645.5	83.5	360	4 US-08-833-752-7	Sequence 7, Appl1
22	1645.5	83.5	360	4 US-09-938-719-7	Sequence 7, Appl1
23	1645.5	83.5	360	4 US-09-939-226B-7	Sequence 7, Appl1
24	1645.5	83.5	360	4 US-09-826-509-473	Sequence 473, App
25	1614.5	82.0	360	3 US-09-045-583-51	Sequence 51, Appl1
26	1614.5	82.0	360	4 US-09-534-185-51	Sequence 51, Appl1
27	1589.5	80.7	347	1 US-08-461-244-3	Sequence 3, Appl1

28	1236	62.7	352	3 US-09-517-605-5	Sequence 5, Appl1
29	1234	62.6	354	3 US-08-724-984A-2	Sequence 2, Appl1
30	1230	62.4	352	3 US-09-045-583-52	Sequence 52, Appl1
31	1230	62.4	352	4 US-09-534-185-52	Sequence 52, Appl1
32	1224	62.1	352	3 US-09-087-232A-13	Sequence 13, Appl1
33	1224	62.1	352	3 US-08-861-105-14	Sequence 14, Appl1
34	1224	62.1	352	3 US-08-575-967A-2	Sequence 2, Appl1
35	1224	62.1	352	4 US-08-833-752-5	Sequence 5, Appl1
36	1224	62.1	352	4 US-09-502-783A-2	Sequence 2, Appl1
37	1224	62.1	352	4 US-09-796-202-1	Sequence 1, Appl1
38	1224	62.1	352	4 US-09-938-719-5	Sequence 5, Appl1
39	1224	62.1	352	4 US-09-502-784A-2	Sequence 2, Appl1
40	1224	62.1	352	4 US-09-339-912A-2	Sequence 2, Appl1
41	1224	62.1	352	4 US-08-771-276-2	Sequence 2, Appl1
42	1224	62.1	352	4 US-08-771-276-20	Sequence 20, Appl1
43	1224	62.1	352	4 US-09-939-226B-5	Sequence 5, Appl1
44	1224	62.1	352	4 US-09-195-662A-2	Sequence 2, Appl1
45	1218	61.8	352	4 US-09-826-509-477	Sequence 477, App

#### ALIGNMENTS

RESULT 1  
US-08-450-393A-2  
; Sequence 2, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Chao, Israel  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coert, Luann  
; REGISTRATION NUMBER: 31,622  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOTIF TYPE: protein  
US-08-450-393A-2

Query Match 100.0%; Score 1970; DB 1; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4,3e-150;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M1STSRSRIRNTNNGEEVTFPDYDYGAPCHKPDKVKGQGLPPLYSIVIFRFGVN 60  
DB 1 M1STSRSRIRNTNNGEEVTFPDYDYGAPCHKPDKVKGQGLPPLYSIVIFRFGVN 60

QY 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
DB 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
QY 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180  
DB 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180  
QY 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWVCSSGILKTLRCRNEKRHR 240  
DB 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWVCSSGILKTLRCRNEKRHR 240  
QY 241 AVRVIETIMIVFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300  
DB 241 AVRVIETIMIVFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300  
QY 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKVKVTTQGLDGRGKXSI 360  
DB 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKVKVTTQGLDGRGKXSI 360  
QY 361 GRAPEASLQDKEGA 374  
DB 361 GRAPEASLQDKEGA 374

## RESULT 2

US-08-446-669-2  
; Sequence 2, Application US/08446669  
; Patent No. 6132987  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Releasee #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,669  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neelley, Richard  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCAL-237/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5000  
; TELEFAX: 415-857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-446-669-2

Query Match 100.0%; Score 1970; DB 3; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4,3e-150;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKPVDKQIGALLPPLYSLVIFGPGVN 60  
|||||

DB 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKPVDKQIGALLPPLYSLVIFGPGVN 60  
QY 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
DB 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
QY 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180  
DB 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180  
QY 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWVCSSGILKTLRCRNEKRHR 240  
DB 181 COKEDSVYVCGPYFPRGMNFTIMRNILGLVPLLIWVCSSGILKTLRCRNEKRHR 240  
QY 241 AVRVIETIMIVFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300  
DB 241 AVRVIETIMIVFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300  
QY 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKVKVTTQGLDGRGKXSI 360  
DB 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKVKVTTQGLDGRGKXSI 360  
QY 361 GRAPEASLQDKEGA 374  
DB 361 GRAPEASLQDKEGA 374

## RESULT 3

US-10-039-659A-14  
; Sequence 14, Application US/10039659A  
; Patent No. 6723520  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Wei  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Vicari, Thomas J.  
; APPLICANT: Schall, Albert  
; APPLICANT: Zlocnik, Albert  
; TITLE OF INVENTION: Antibodies that bind chemokine TECK  
; FILE REFERENCE: DX0589K1B US  
; CURRENT APPLICATION NUMBER: US/10/039,659A  
; PRIOR FILING DATE: 2002-01-03  
; PRIOR APPLICATION NUMBER: US 08/887,977  
; PRIOR FILING DATE: 1997-07-03  
; PRIOR APPLICATION NUMBER: US 60/021,664  
; PRIOR FILING DATE: 1996-07-05  
; PRIOR APPLICATION NUMBER: US 60/028,329  
; PRIOR FILING DATE: 1996-10-11  
; PRIOR APPLICATION NUMBER: US 60/048,593  
; PRIOR FILING DATE: 1997-06-04  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 14  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-039-659A-14

Query Match 100.0%; Score 1970; DB 4; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4,3e-150;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKPVDKQIGALLPPLYSLVIFGPGVN 60  
DB 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKPVDKQIGALLPPLYSLVIFGPGVN 60  
QY 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
DB 61 MLVVLILNCKKLCJTDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNACKLFTGLY 120  
QY 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180  
DB 121 HIGYGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using SW model

Run on: November 1, 2005, 21:08:32 ; Search time 40 Seconds

(without alignments)  
899,627 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 M1STSRSRFRINTNESGEEV.....GKGSIGRAPEASTQDEKA 374

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	2 I38450	chemokine (C-C) re
2	1651.5	83.8	360	2 UC2443	chemokine (C-C) re
3	1224	62.1	352	2 A43113	chemokine (C-C) re
4	967.5	49.1	355	2 A45177	chemokine (C-C) re
5	960	48.7	359	2 I49341	MIP-1 alpha receptor
6	902.5	45.8	355	2 I49339	macrophage inflam
7	890.5	45.2	355	2 G02436	chemokine (C-C) re
8	833	42.3	360	2 UC4587	chemokine (C-C) re
9	831.5	42.2	360	2 A57160	chemokine (C-C) re
10	794.5	40.3	363	2 S55594	G protein-coupled
11	731	37.1	356	2 I49340	MIP-1 alpha recept
12	723	36.7	355	2 UC5067	G protein-coupled
13	704.5	35.8	354	2 I58186	probable G protein
14	698	35.4	355	2 UC4504	orphan G protein-c
15	644.5	32.7	344	2 UC5942	chemokine receptor
16	584	29.6	378	2 B55735	lymphocyte-specifi
17	575.5	29.2	378	2 A55735	G protein-coupled
18	570	28.9	378	2 A45680	G protein-coupled
19	554.5	28.1	369	2 UC5068	G protein-coupled
20	541.5	27.5	360	2 A53611	interleukin-8 rece
21	537	27.3	359	2 A48921	interleukin-8 rece
22	530.5	26.9	353	2 G00048	neuropeptide Y/pep
23	529.5	26.9	355	2 S28787	neuropeptide Y/pep
24	529.5	26.9	355	2 S28787	neuropeptide Y/pep
25	526	26.8	352	2 A53752	interleukin-8 rece
26	526	26.7	358	2 A53752	interleukin-8 rece
27	526	26.6	357	2 UC0349	interleukin-8 rece
28	524.5	26.6	356	2 A39445	interleukin-8 rece
29	523	26.5	356	2 S42096	interleukin-8 rece

30	519	26.3	333	2 I65989	G protein-coupled
31	484	24.6	350	2 JN0621	G protein-coupled
32	480	24.4	359	2 A42556	angiotensin II rec
33	479.5	24.3	374	2 S42628	G protein-coupled
34	475	24.1	359	2 I51372	angiotensin II rec
35	473	24.0	359	2 UC2134	angiotensin II rec
36	472	23.9	359	2 JH0621	angiotensin II rec
37	471	23.9	359	2 S15403	angiotensin II rec
38	471	23.9	359	2 JQ1516	angiotensin II rec
39	469	23.8	359	2 UC1104	angiotensin II rec
40	468	23.8	359	2 S44425	angiotensin II rec
41	465	23.6	359	2 UC1194	angiotensin II rec
42	465	23.6	374	2 S32785	G protein-coupled
43	464	23.6	359	2 A48857	angiotensin II rec
44	461.5	23.4	327	2 S26667	G protein-coupled
45	460.5	23.4	327	2 S56162	MDCK15 protein - h

## ALIGNMENTS

## RESULT 1

I38450

chemokine (C-C) receptor 2, splice form A - human

N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte che

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004

C/Accession: I38450

R/Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A/Title: Molecular cloning and functional expression of two monocyte chemoattractant pr

A/Reference number: A53477; NCID:94195821; PMID:8146186

A/Accession: I38450

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-374 &lt;RES&gt;

A/Cross-references: UNIPROT:P41597; EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472

C/Genetics:

A/Gene: GDB:CMKBR2

A/Cross-references: GDB:337364; OMIM:601267

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	M1STSRSRFRINTNESGEEVTTTFDYDYGAPCHKEFVKQIGAOQLPLPLSLVIRFVGN	60
DB	1	M1STSRSRFRINTNESGEEVTTTFDYDYGAPCHKEFVKQIGAOQLPLPLSLVIRFVGN	60
QY	61	MLVVLILNCKKLCCLTDIYLNLAISDLFLITLPLMAHSANENVPFGAMCKLFTGLY	120
DB	61	MLVVLILNCKKLCCLTDIYLNLAISDLFLITLPLMAHSANENVPFGAMCKLFTGLY	120
QY	121	HIGYFGIFFIILITDRYLAIVHAFALKARTVTFVTSVITWLVAFASVPGIIFTK	180
DB	121	HIGYFGIFFIILITDRYLAIVHAFALKARTVTFVTSVITWLVAFASVPGIIFTK	180
QY	181	CKEDSVYVCGPFPPGAMNFFRTIMNIIIGLVPLIIMVTCISGILKTLRCNEKKRR	240
DB	181	CKEDSVYVCGPFPPGAMNFFRTIMNIIIGLVPLIIMVTCISGILKTLRCNEKKRR	240
QY	240	181	CKEDSVYVCGPFPPGAMNFFRTIMNIIIGLVPLIIMVTCISGILKTLRCNEKKRR
DB	240	181	CKEDSVYVCGPFPPGAMNFFRTIMNIIIGLVPLIIMVTCISGILKTLRCNEKKRR

Qy	241	AVRVIETIMIVYFLPWTPEYINVLILNTQEPFGSGNCSSTQLDQAQTVEETLMTHTCCI	300
Db	241	AVRVIFITMIVYFLPWTPEYINVLILNTQEPFGSLNCSTSQLDAQTVEETLMTHTCCI	300
Qy	301	NPIIYAFAFGEKFRSLFHIALGRIAPLPVCGGGGVARGKNVYVTTOGLLDGRGKGSKI	360
Db	301	NPIIYAFAFGEKFRSLFHIALGRIAPLPVCGGGGVARGKNVYVTTOGLLDGRGKGSKI	360
Qy	361	GRAPEASTLODKEGA	374
Db	361	GRAPEASTLODKEGA	374

## RESULT 2

N:Alternate names: C-C-CR-2, monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C-receptor 2, splice form B - human)  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C:Accession: J02443; J18463  
 R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
 A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein  
 A:Reference number: J02443; MUID:94324942; PMID:8048929  
 A:Accession: J02443  
 A:Reference number: J02443  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <RMS>  
 A:Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:G531246; PIDN:AAA06253.1; PID:G531246; R:Chiaro, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein  
 A:Reference number: A53477; MUID:94195821; PMID:8146186  
 A:Accession: J18463  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <RES>  
 A:Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558  
 C:Genetics:  
 A:Gene: GDB:CMKBR2  
 A:Cross-references: GDB:337364; OMIM:601267  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
 F:41-70/Domain: transmembrane #status predicted <TM1>  
 F:81-100/Domain: transmembrane #status predicted <TM2>  
 F:115-116/Domain: transmembrane #status predicted <TM3>  
 F:154-178/Domain: transmembrane #status predicted <TM4>  
 F:207-226/Domain: transmembrane #status predicted <TM5>  
 F:244-268/Domain: transmembrane #status predicted <TM6>  
 F:287-309/Domain: transmembrane #status predicted <TM7>  
 F:114/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:114-190/Dsulfide bonds: #status predicted

Query Match	83.8%	Score 1651.5	DB 2	Length 360
Best Local Similarity	95.5%	Pred. No. 7.1e-137		
Matches 319, Conservative		3, Mismatches 5	Indels 7	Gaps 3

Qy	1	MLSTSRSPFINNTNNESSGEVTTFFPDYDGAQCHKFDVQIAQOLLPPLXSLVFIFFGFNGN	60
Db	1	MLSTSRSPFINNTNNESSGEVTTFFPDYDGAQCHKFDVQIAQOLLPPLXSLVFIFFGFNGN	60
Qy	61	MLVVLILINCKKTKCLTDIYLLNLAIASDLLELTPLPLMAHSAANEWFGNACMLFTGLY	120
Db	61	MLVVLILINCKKTKCLTDIYLLNLAIASDLLELTPLPLMAHSAANEWFGNACMLFTGLY	120
Qy	121	HIGYFGGIFPIILLTIDRYLAIIVHAVFALKARTYVFGVTSVITWLVAVFASVPGIILFTK	180
Db	121	HIGYFGGIFPIILLTIDRYLAIIVHAVFALKARTYVFGVTSVITWLVAVFASVPGIILFTK	180
Qy	181	CQKEDSVVVCGRPYPRGNNNFHTIMRNILGLVPLILINVCYSGILKTLILACRNEKKRRH	240
Db	181	CQKEDSVVVCGRPYPRGNNNFHTIMRNILGLVPLILINVCYSGILKTLILACRNEKKRRH	240

QY	241	AVRVLFTIMVYFLFWETRYNYIVILANTQEPFGSLNCSTSLQDQATQVETLGMHCCI	300
QY	241	AVRVLFTIMVYFLFWETRYNYIVILANTQEPFGSLNCSTSLQDQATQVETLGMHCCI	300
Db	241	AVRVLFTIMVYFLFWETRYNYIVILANTQEPFGSLNCSTSLQDQATQVETLGMHCCI	300
QY	301	NPITVAVVEGKFR---SLP---HIALG-CRIAPL	327
Db	301	NPITVAVVEGKFRRLYSVFRKHINRKCKOCPP	334

## RESULT 3

chemokine (C-C receptor 5 - human  
N.Alternate names: C-C CR-5; CCR5  
C.Species: Homo sapiens (man)  
C.Date: 12-Jul-1996 #sequence, revision 12-Jul-1996 #text change 20-Jun-2000  
A.Accession: A4J113; S11808; AS8834; AS8832; G02653; AS8833  
R.Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A.Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A.Reference number: A4J113; PMID:96241590; PMID:8659485  
A.Accession: A4J113  
A.Molecule type: mRNA  
A.Residues: 1-352 <SAML>  
A.Cross-references: GB:X91492; NID:g1262810; PIDN:CA62796.1; PID:g1262811  
R.Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragost  
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa  
Nature 382, 722-725, 1996  
A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o  
A.Reference number: S71808; PMID:96345670; PMID:8751444  
A.Accession: S71808  
A.Status: nucleic acid sequence not shown; not compared with conceptual translation  
A.Molecule type: DNA  
A.Accession: AS8834  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A.Molecule type: DNA  
A.Residues: 1-184; 'IKDSHLGAGPAAACGHLLGNPKNSASVSK' <SAM3>  
A.Cross-references: GB:X93933; NID:g1524062; PIDN:CA657767.1; PID:g1524063  
A.Note: this frameshift mutation results in a non-functional receptor but confers a degre  
nd may have had a selective advantage by conferring resistance to Yersinia plague infect  
R.Combadere, C.; Ahuja, S.K.; Tilfany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec  
A.Reference number: AS8832; PMID:96295970; PMID:8699119  
A.Accession: AS8832  
A.Molecule type: mRNA  
A.Residues: 1-352 <COM1>  
A.Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409  
A.Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R.Combadere, C.  
submitted to the EMBL Data Library, May 1996  
A.Reference number: H01541  
A.Accession: G02653  
A>Status: translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-89; 'I', 'I', '352 <COM2>  
A.Cross-references: EMBL:U57840  
A.Rapoport, C.J.; Gosling, J.; Schwelckart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A>Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A.Reference number: AS8833; PMID:96291862; PMID:8663314  
A.Accession: AS8833  
A.Molecule type: mRNA  
A.Residues: 1-352 <RAP>  
A.Cross-references: GB:U54994; NID:g1457945; PIDN:AAC05098.1; PID:g1457946  
C.Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see  
C.Genetics: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C  
A.Gene: GDB:CMKR5; CCR5; CR-5; CC-CCR-5; CCR5; Chem13  
A.Cross-references: GDB:I230510; OMIM:601373  
A.Map position: 3p21-3p21  
C.Function:  
A.Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 21:00:15 ; Search time 173 Seconds

(without alignments)  
1107.038 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 MLSTSRSRFRIRNTNSESSEV.....GKGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	374	1	CKR2_HUMAN
2	1614.5	82.0	360	1	CKR2_MACMU
3	1346.5	68.4	373	1	CKR2_RAT
4	1332.5	67.6	373	1	CKR2_MOUSE
5	1327.5	67.4	373	2	Q6Y742
6	1252	63.6	352	2	Q95NC2
7	1247	63.3	352	2	Q68G28
8	1244	63.1	339	2	Q9TGT3
9	1244	63.1	339	2	Q9TUV8
10	1244	63.1	332	2	Q6WV98
11	1244	63.1	352	2	Q9MZA0
12	1243	63.1	354	1	CKR5_MOUSE
13	1243	63.1	339	2	Q9TGV5
14	1243	63.1	352	2	Q95NC4
15	1241	63.0	352	2	Q6WV93
16	1241	63.0	352	2	Q6WV96
17	1241	63.0	352	2	Q6WV97
18	1240	62.9	339	2	Q9TUV0
19	1239	62.9	352	2	Q6Y741
20	1239	62.9	352	2	Q9M299
21	1238.5	62.9	339	2	Q9TUV6
22	1238	62.8	339	2	Q9TUV1
23	1237	62.8	339	2	Q9TUV9
24	1236	62.7	339	2	Q9TUV0
25	1236	62.7	352	1	CKR5_CERTO
26	1236	62.7	352	1	CKR5_CERTO
27	1236	62.7	352	2	Q6WV92
28	1236	62.7	352	2	Q6WV94
29	1236	62.7	352	2	Q71RS2
30	1236	62.7	352	2	Q71RS2
31	1235	62.7	339	2	Q9T5N3

32	1235	62.7	352	2	077776	077776	cercopithec
33	1234	62.6	339	2	Q9TUV5	Q9TUV5	sagittinus sp
34	1234	62.6	352	2	Q6WV95	Q6WV95	leontopithec
35	1233	62.6	339	2	Q9TUV2	Q9TUV2	alouatta ca
36	1233	62.6	352	2	Q95NE1	Q95NE1	cercopithec
37	1232	62.5	339	2	Q9TUV9	Q9TUV9	macaca mula
38	1232	62.5	339	2	Q9TUV0	Q9TUV0	actus trivi
39	1232	62.5	339	2	Q9TUV4	Q9TUV4	callithrix
40	1232	62.5	339	2	Q9TUV0	Q9TUV0	hylobates c
41	1232	62.5	332	2	Q6WV91	Q6WV91	brachyteles
42	1231	62.5	339	2	Q9TUV9	Q9TUV9	hylobates c
43	1231	62.5	352	1	CKR5_HYLM1	Q95NC0	hylobates m
44	1231	62.5	352	2	Q95NC9	Q95NC9	alouatta se
45	1231	62.5	352	2	Q9XT12	Q9XT12	cercopithec

## ALIGNMENTS

RESULT 1

ID	CKR2_HUMAN	STANDARD	PRT	374 AA.
AC	P41597			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)			
DE	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).			
GN	Name=CCR2; Synonyms=CMKBR2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94195821; PubMed=8146186;			
RA	Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,			
RA	Coughlin S.R.,			
RT	"Molecular cloning and functional expression of two monocyte			
RT	chemoattractant protein 1 receptors reveals alternative splicing of			
RT	the carboxyl-terminal tails."			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94324942; PubMed=8048929;			
RA	Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;			
RA	"cDNA cloning and functional expression of a human monocyte			
RT	chemoattractant protein 1 receptor."			
RL	Biochem. Biophys. Res. Commun. 202:1156-1162(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;			
RA	Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Charo I.F.;			
RT	"Organization and differential expression of the human monocyte			
RT	chemoattractant protein 1 receptor gene. Evidence for the role of the			
RT	carboxyl-terminal tail in receptor trafficking."			
RL	J. Biol. Chem. 272:1038-1045(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,			
RA	Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,			
RA	Gao J., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,			
RA	Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,			
RA	Dragan V., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,			
RA	Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,			
RA	Sagripanti J.L.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,			
RA	Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;			
RT	"SeattleSNP. NHLBI HL6682 program for genomic applications, UW-			
RT	FHCRC, Seattle, WA (URL: <a href="http://pga.gs.washington.edu">http://pga.gs.washington.edu</a> )."			



RU Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 [6]  
 RN SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
 RP MEDLINE=20501139; PubMed=11046064;  
 RA Predobrazhensky A.A., Drogan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
 RA Chakravarty L., Koliatukudy P.E.,  
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
 RT has tyrosine sulfation in a conserved extracellular N-terminal  
 RT region.";  
 RT J. Immunol. 165:5295-5303 (2000).  
 CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=P41597-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P41597-2; Sequence=VSP\_001893;  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, U03882; AAA19119.1; -  
 DR EMBL, U03905; AAA19120.1; -  
 DR EMBL, D29984; BAA06253.1; -  
 DR EMBL, U80924; AAC1637.1; -  
 DR EMBL, U80924; AAC1636.1; -  
 DR EMBL, U95626; AAB57791.1; -  
 DR EMBL, U95626; AAB57792.1; -  
 DR EMBL, AF545480; AAN16400.1; -  
 DR PIR, J38443; J38450.  
 DR PIR, J38443; J38443.  
 DR PDB, 1KAD; Model, A=1-349.  
 DR PDB, 1KPI; Model, A=1-349.  
 DR Genew; HGNC:1603; CCR2.  
 DR MIM; 601267; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.  
 DR GO; GO:0019735; F:antimicrobial humoral response (sensu Verte. .); TAS.  
 DR GO; GO:0006968; P:cellular defense response; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.  
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.  
 DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. .; TAS.  
 DR InterPro; IPR002237; CC\_2 receptor.  
 DR InterPro; IPR000355; Chemkin receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW 3D-structure; Alternative splicing; G-protein coupled receptor;  
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.  
 FT DOMAIN 1 42 Extracellular (Potential).  
 FT TRANSMEM 43 70 1 (Potential).  
 FT DOMAIN 71 80 Cytoplasmic (Potential).  
 FT TRANSMEM 81 100 2 (Potential).  
 FT DOMAIN 101 114 Extracellular (Potential).  
 FT TRANSMEM 115 136 3 (Potential).  
 FT DOMAIN 137 153 Cytoplasmic (Potential).  
 FT TRANSMEM 154 178 4 (Potential).  
 FT DOMAIN 179 206 Extracellular (Potential).  
 RT

FT TRANSMEM 207 226 5 (Potential).  
 FT DOMAIN 227 243 Cytoplasmic (Potential).  
 FT TRANSMEM 244 268 6 (Potential).  
 FT DOMAIN 269 285 Extracellular (Potential).  
 FT TRANSMEM 286 309 7 (Potential).  
 FT DOMAIN 310 374 Cytoplasmic (Potential).  
 FT CAROXYD 14 14 N-linked (GlcNAc. . .) (Potential).  
 FT MOD RES 26 26 Sulfotyrosine.  
 FT DISULFID 113 190 By similarity.  
 FT VARSPLC 314 374 SLFHALGRIAPLQKPGVGVRGKRVKTTGSLDGR  
 GKGKSGRAPASLQDXEGA -> RYLSVFRKHTTKRCK  
 QCVFRTVDGVSTINPSTGEQVSAKL (in  
 isoform B).  
 FT FTId=VSP\_001893.  
 FT V -> I (in dbSNP:1799864).  
 FT FTId=VAR\_014339.  
 FT VARIANT 64 64 /FTId=VAR\_014339.  
 FT VARIANT 355 355 G -> E.  
 FT FTId=VAR\_014340.  
 FT FTId=VAR\_014340.  
 FT SQ SEQUENCE 374 AA; 41914 MW; F865E0D3E74CF0F CRC64;  
 Query Match 100.0%; Score 1970; DB 1; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 1e-118;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSPFRINTNMSGSEVTFPDYDYGAPCHKFDVQIGAQLLPPLYSLVIFGVGN 60  
 DB 1 MLSTSRSPFRINTNMSGSEVTFPDYDYGAPCHKFDVQIGAQLLPPLYSLVIFGVGN 60  
 QY 61 MLVYLILNCKKCKLTITLILNLAISDLLFLITPLVAHSAANWVGNNACKLFTGLY 120  
 DB 61 MLVYLILNCKKCKLTITLILNLAISDLLFLITPLVAHSAANWVGNNACKLFTGLY 120  
 QY 121 HIGYFGGIFFIILITIDRYLAIVHVPALKARTVFGVTSVITMLVAVFASVPGIIFPK 180  
 DB 121 HIGYFGGIFFIILITIDRYLAIVHVPALKARTVFGVTSVITMLVAVFASVPGIIFPK 180  
 QY 181 COKEDSVYVCGPYPRGNNPHTIRNITGLVPLLIIVICYSGLIKTLRCRNEKRRR 240  
 DB 181 COKEDSVYVCGPYPRGNNPHTIRNITGLVPLLIIVICYSGLIKTLRCRNEKRRR 240  
 QY 241 AVRVIETIMIVYFLPWTYRNIVILNTOEPFGNSCESTSLDQATOVETILGMTHCI 300  
 DB 241 AVRVIETIMIVYFLPWTYRNIVILNTOEPFGNSCESTSLDQATOVETILGMTHCI 300  
 QY 301 NPIIYAFYGEKFRSLFIHALGRIAPLQKPGVGVRGKRVKTTGSLDGRGKXSI 360  
 DB 301 NPIIYAFYGEKFRSLFIHALGRIAPLQKPGVGVRGKRVKTTGSLDGRGKXSI 360  
 QY 361 GRAPEASLQDXEGA 374  
 DB 361 GRAPEASLQDXEGA 374  
 RESULT 2  
 CCR2\_MACMU STANDARD; PRT; 360 AA.  
 ID CCR2\_MACMU  
 AC 018793;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CR-2) (CCR-2) (CCR2)  
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
 GN Name=CCR2; Synonyms=CMKBR2;  
 OS Macaca mulatta (rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9544;  
 RN NCBI\_TaxID=9544;  
 RP [1]  
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/089822201750290104;  
 RA Margulies B.J., Hauer D.A., Clements J.E.,  
 RT "Identification and comparison of eleven rhesus macaque chemokine





Db 61 MLVVLILNCKKLCITDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYGGIFETILLTDRILAVHVPALKARTVFGVTSYITMLVANFASVPGIIFPK 180  
Db 121 HIGYGGIFETILLTDRILAVHVPALKARTVFGVTSYITMLVANFASVPGIIFPK 180  
QY 181 COKEDSVYVCGPYFPRGMNFFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRR 240  
Db 181 COKEDSVYVCGPYFPRGMNFFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRR 240  
QY 241 AVRVIETIMIVFLFTPNIVILNTFOEFGLSNCESTSQLDQATQVETILGTHCCI 300  
Db 241 AVRVIETIMIVFLFTPNIVILNTFOEFGLSNCESTSQLDQATQVETILGTHCCI 300  
QY 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGGPGVRGKVKVTTQGLDGRGKSI 360  
Db 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGGPGVRGKVKVTTQGLDGRGKSI 360  
QY 361 GRAPEASLODKEGA 374  
Db 361 GRAPEASLODKEGA 374

## RESULT 2

US-10-039-659-14

; Sequence 14, Application US/10039659

; Publication No. US20030018167A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Wei

; Glash, Kurt C.

; Schall, Thomas J.

; Vicari, Alain P.

; Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/039,659

; FILING DATE: 03-Jan-2002

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/887,977

; FILING DATE: 03-JUL-1997

; APPLICATION NUMBER: US 60/021,644

; FILING DATE: 05-JUL-1996

; APPLICATION NUMBER: US 60/028,329

; FILING DATE: 11-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0589K1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9192

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 374 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-039-659-14

Query Match 100.0%; Score 1970; DB 14; Length 374;

Best Local Similarity 100.0%; Pred. No. 3.7e-163; Indels 0; Gaps 0;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLSLVFIQFVGN 60  
Db 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLSLVFIQFVGN 60  
QY 61 MLVVLILNCKKLCITDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNAMCKLFTGLY 120  
Db 61 MLVVLILNCKKLCITDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYGGIFETILLTDRILAVHVPALKARTVFGVTSYITMLVANFASVPGIIFPK 180  
Db 121 HIGYGGIFETILLTDRILAVHVPALKARTVFGVTSYITMLVANFASVPGIIFPK 180  
QY 181 COKEDSVYVCGPYFPRGMNFFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRR 240  
Db 181 COKEDSVYVCGPYFPRGMNFFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRR 240  
QY 241 AVRVIETIMIVFLFTPNIVILNTFOEFGLSNCESTSQLDQATQVETILGTHCCI 300  
Db 241 AVRVIETIMIVFLFTPNIVILNTFOEFGLSNCESTSQLDQATQVETILGTHCCI 300  
QY 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGGPGVRGKVKVTTQGLDGRGKSI 360  
Db 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGGPGVRGKVKVTTQGLDGRGKSI 360  
QY 361 GRAPEASLODKEGA 374  
Db 361 GRAPEASLODKEGA 374

## RESULT 3

US-10-239-423-63

; Sequence 63, Application US/10239423

; Publication No. US20030186889A1

; GENERAL INFORMATION:

; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ABERMANN, Knut;

; HEITLAND, Alexandra; SPODSBERG, Nikolaj

; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and

; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,

; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction

; FILE REFERENCE: 02221708

; CURRENT APPLICATION NUMBER: US/10/239,423

; CURRENT FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: DE10016013.1

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies

; US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;

Best Local Similarity 100.0%; Pred. No. 3.7e-163; Indels 0; Gaps 0;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLSLVFIQFVGN 60  
Db 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLSLVFIQFVGN 60  
QY 61 MLVVLILNCKKLCITDIYLLNLAIISDLLFLITLPLMAHSAANEVFGNAMCKLFTGLY 120